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Amendments to the Claims:

Claims 1-61 (Cancelled)

62. (New) A method for altering the disulfide status of storage proteins in a plant or part thereof, said method comprising transforming said plant with a first nucleotide construct comprising a first nucleotide sequence and a second nucleotide construct comprising a second nucleotide sequence,

wherein said first nucleotide sequence encodes an NADPH-thioredoxin reductase, said second nucleotide sequence encodes a thioredoxin *h*, and said first nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 24;
- b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 25;
- c) a nucleotide sequence having at least 95% sequence identity to the coding sequence of the nucleotide sequence set forth in SEQ ID NO: 24;
- d) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO: 24; and
- e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d);

wherein said disulfide status of said storage proteins is altered in said plant or part thereof.

63. (New) The method of claim 62, wherein said second nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 13;
- b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 14;
- c) a nucleotide sequence having at least 95% sequence identity to the coding sequence of the nucleotide sequences set forth in SEQ ID NO: 13;

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d) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO: 13; and

e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d).

64. (New) The method of claim 62, wherein said part is seed or grain.

65. (New) The method of claim 62, wherein at least one of said first and said second nucleotide constructs further comprises an operably linked promoter that drives expression in a plant cell.

66. (New) The method of claim 65, wherein said promoter is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.

67. (New) A method for improving the digestibility of grain, said method comprising transforming a plant with a first nucleotide construct comprising a first promoter that drives expression in a plant cell operably linked to a first nucleotide sequence and a second nucleotide construct comprising a second promoter that drives expression in a plant cell operably linked to a second nucleotide sequence,

wherein said first nucleotide sequence encodes an NADPH-thioredoxin reductase, said second nucleotide sequence encodes a thioredoxin *h*, and said first nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 24;
- b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 25;
- c) a nucleotide sequence having at least 95% sequence identity to the coding sequence of the nucleotide sequence set forth in SEQ ID NO: 24;
- d) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO: 24; and

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e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d);
wherein said digestibility of said grain is increased when consumed by an animal.

68. (New) The method of claim 67, wherein said second nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 13;
- b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 14;
- c) a nucleotide sequence having at least 95% sequence identity to the coding sequence of the nucleotide sequences set forth in SEQ ID NO: 13;
- d) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO: 13; and
- e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d).

69. (New) The method of claim 67, wherein at least one of said first and said second promoters is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.

70. (New) The method of claim 67, wherein said animal is a ruminant animal or a monogastric animal.

71. (New) The method of claim 67, wherein the grain is a mature maize kernel.

72. (New) The method of claim 67, wherein the grain is a kernel that is part of whole plant corn harvested for silage.

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73. (New) A method for improving grain for processing, said method comprising transforming a plant with a first nucleotide construct comprising a first promoter that drives expression in a plant cell operably linked to a first nucleotide sequence and a second nucleotide construct comprising a second promoter that drives expression in a plant cell operably linked to a second nucleotide sequence,

wherein said first nucleotide sequence encodes an NADPH-thioredoxin reductase, said second nucleotide sequence encodes a thioredoxin *h*, and said first nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 24;
 - b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 25;
 - c) a nucleotide sequence having at least 95% sequence identity to the coding sequence of the nucleotide sequence set forth in SEQ ID NO: 24;
 - d) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO: 24; and
 - e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d);
- wherein said grain is improved for processing.

74. (New) The method of claim 73, wherein said second nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 13;
- b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 14;
- c) a nucleotide sequence having at least 95% sequence identity to the coding sequence of the nucleotide sequences set forth in SEQ ID NO: 13;
- d) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO: 13; and
- e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d).

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75. (New) The method of claim 73, wherein at least one of said first and said second promoters is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.

76. (New) The method of claim 73, wherein the processing is wet milling and the improvement is increased starch extractability, decreased need for chemical reducing agents, or improved digestibility of wet milling by-products.

77. (New) The method of claim 73, wherein the processing is grinding and the improvement is a higher degree of particle size reduction or energy savings.

78. (New) The method of claim 73, wherein the processing is steam flaking and the improvement is a larger improvement in digestibility enhancement by steam flaking or energy savings.

79. (New) The method of claim 73, wherein the processing is dry grind ethanol production and the improvement is increased fermentable starch or increased digestibility of fermentation by-products.

80. (New) A method for altering the disulfide status of storage proteins in a plant or part thereof, said method comprising transforming said plant with a first nucleotide construct comprising a first nucleotide sequence and a second nucleotide construct comprising a second nucleotide sequence, wherein said first nucleotide sequence encodes an NADPH-thioredoxin reductase and said second nucleotide sequence encodes a thioredoxin *h*, and wherein said disulfide status of said storage proteins is altered in said plant or part thereof.

81. (New) The method of claim 80, wherein said part is seed or grain.

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82. (New) The method of claim 80, wherein at least one of said first and said second nucleotide constructs further comprises an operably linked promoter that drives expression in a plant cell.

83. (New) The method of claim 82, wherein said promoter is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.

84. (New) The method of claim 80, wherein the digestibility of said grain is increased when consumed by an animal.

85. (New) The method of claim 80, wherein the hardness of said grain is increased or decreased.

86. (New) The method of claim 80, wherein said grain is improved for processing.

87. (New) A transformed plant comprising stably incorporated in its genome a first nucleotide construct comprising a first promoter that drives expression in a plant cell operably linked to a first nucleotide sequence and a second nucleotide construct comprising a second promoter that drives expression in a plant cell operably linked to a second nucleotide sequence,

wherein said first nucleotide sequence encodes an NADPH-thioredoxin reductase, said second nucleotide sequence encodes a thioredoxin *h*, and said first nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 24;
- b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 25;
- c) a nucleotide sequence having at least 95% sequence identity to the coding sequence of the nucleotide sequence set forth in SEQ ID NO: 24;

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- d) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO: 24; and
- e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d);

88. (New) The plant of claim 87, wherein said second nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence set forth in SEQ ID NO: 13;
- b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 14;
- c) a nucleotide sequence having at least 95% sequence identity to the coding sequence of the nucleotide sequences set forth in SEQ ID NO: 13;
- d) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence set forth in SEQ ID NO: 13; and
- e) a nucleotide sequence that is complementary to the nucleotide sequence of a), b), c), or d).

89. (New) The plant of claim 87, wherein said promoter is selected from the group consisting of seed-preferred, constitutive, chemically regulated, tissue-preferred, and developmentally regulated promoters.

90. (New) The plant of claim 87, wherein said plant is a monocot.

91. (New) The plant of claim 90, wherein said monocot is selected from the group consisting of maize, wheat, rice, sorghum, barley, millet and rye.

92. (New) The plant of claim 87, wherein said plant is a dicot.

93. (New) The plant of claim 92, wherein said dicot is selected from the group consisting of soybean, *Brassica sp.*, alfalfa, safflower, sunflower, cotton, peanut and potato.

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94. (New) Transformed seed of the plant of claim 87.